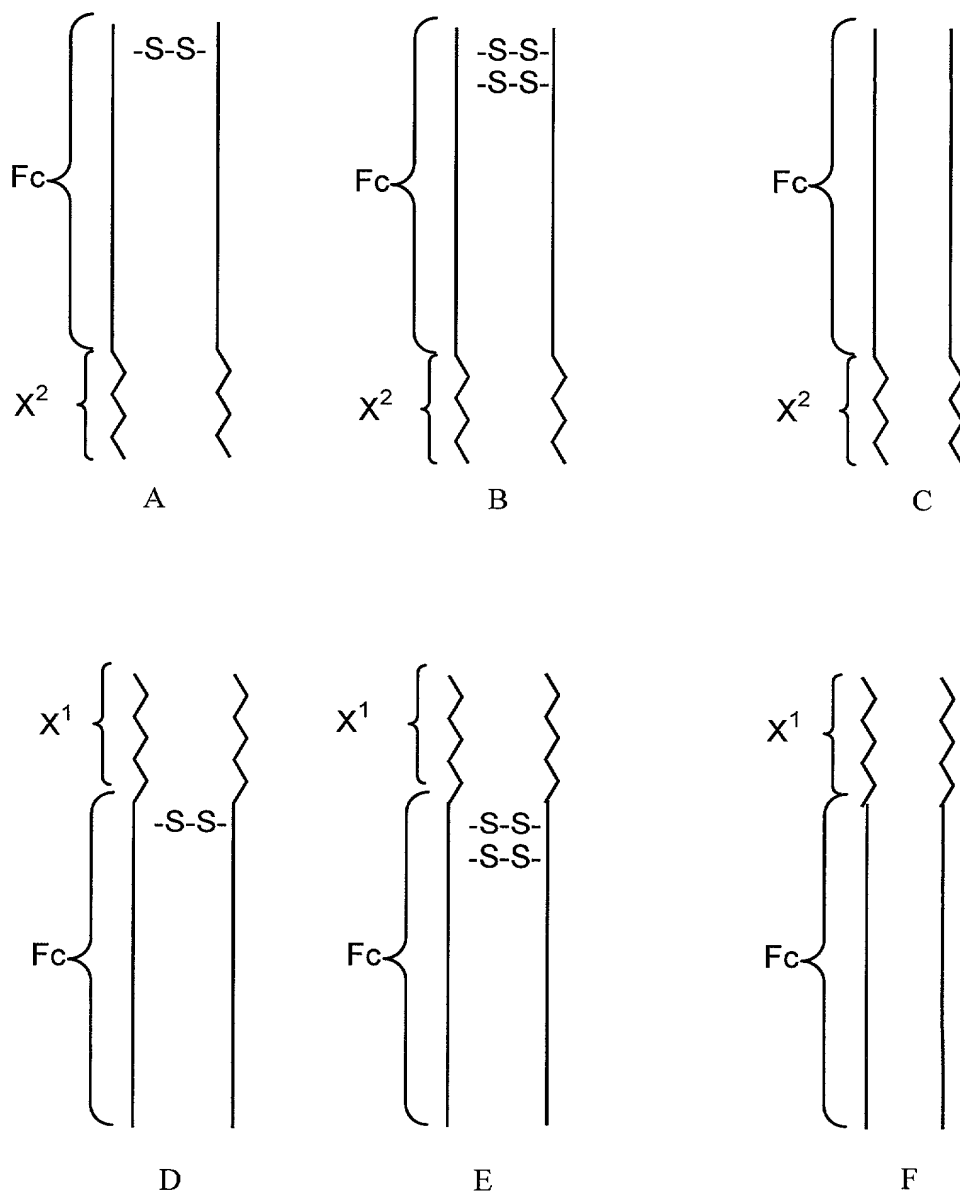
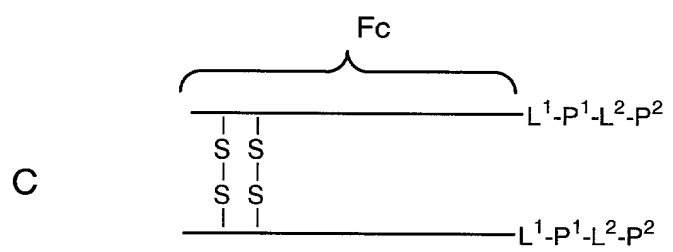
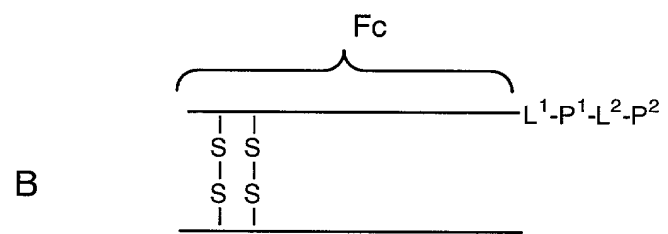
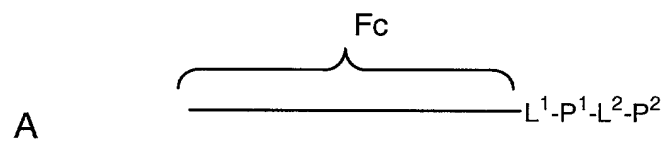


FIGURE 1



**FIGURE 2**



**FIGURE 3A**

```

ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCGTCA
1  -----+-----+-----+-----+-----+-----+-----+ 60
TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT

a   M   D   K   T   H   T   C   P   P   C   P   A   P   E   L   L   G   G   P   S   -

GTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
61  -----+-----+-----+-----+-----+-----+-----+ 120
CAGAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG

a   V   F   L   F   P   P   K   P   K   D   T   L   M   I   S   R   T   P   E   V   -

ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 -----+-----+-----+-----+-----+-----+-----+ 180
TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a   T   C   V   V   V   D   V   S   H   E   D   P   E   V   K   F   N   W   Y   V   -

GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
181 -----+-----+-----+-----+-----+-----+-----+ 240
CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC

a   D   G   V   E   V   H   N   A   K   T   K   P   R   E   E   Q   Y   N   S   T   -

TACCGTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 -----+-----+-----+-----+-----+-----+-----+ 300
ATGGCACACCAGTCGCGAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCCTTCCTCATG

a   Y   R   V   V   S   V   L   T   V   L   H   Q   D   W   L   N   G   K   E   Y   -

AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCC
301 -----+-----+-----+-----+-----+-----+-----+ 360
TTCACGTTCAGAGGTGTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG

a   K   C   K   V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   A   -

AAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACC
361 -----+-----+-----+-----+-----+-----+-----+ 420
TTTCCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG

a   K   G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L   T   -

AAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
421 -----+-----+-----+-----+-----+-----+-----+ 480
TTCTTGGTCCAGTCGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D   I   A   V   -

GAGTGGGAGAGCAATGGGCAGCCGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGAC
481 -----+-----+-----+-----+-----+-----+-----+ 540
CTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAGGACCTG

a   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T   P   P   V   L   D   -

TCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC

a   S   D   G   S   F   F   L   Y   S   K   L   T   V   D   K   S   R   W   Q   Q   -

GGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 -----+-----+-----+-----+-----+-----+-----+ 660
CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC

a   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   K   -

```

**FIGURE 3B**

```
661  AGCCTCTCCCTGTCTCCGGGTAAA 684
      -----+-----+-----
      TCGGAGAGGGACAGAGGCCCATTT
a      S  L  S  L  S  P  G  K
```